

Amendments to the Specification:

Please insert the following table at line 25, page 23 of the specification:

TABLE 1

RNA fragment No	nucleotides	Kd <sub>app</sub> (in nM)
1, SEQ. ID NO. 15	UUUUUUUU	not bound
2, SEQ. ID NO. 16	UUUUUUUU	0.97 +/- 0.19
3, SEQ. ID NO. 17	(AUUU) <sub>2</sub> A	not bound
4a, SEQ. ID NO. 18	(AUUU) <sub>3</sub> A	1.40 +/- 0.39
4a, SEQ. ID NO. 19	AUUIAUUUAUUU <u>A</u>	not bound
4b, SEQ. ID NO. 20	AUUUAUUUAUUUA	0.77 +/- 0.25
4c, SEQ. ID NO. 21	AUU <u>A</u> UU <u>A</u> UUUA	not bound
4d, SEQ. ID NO. 22	AUU <u>A</u> UU <u>A</u> UUUA	not bound
prel.consensus	N N U/C U N N U/C U U/C	
7a, SEQ. ID NO. 23	U <u>A</u> UUUUUU	not bound
7b, SEQ. ID NO. 24	UA <u>A</u> UUUUU	not bound
7c, SEQ. ID NO. 25	UAUUUU <u>A</u> U	not bound
7d, SEQ. ID NO. 26	UAUUUU <u>A</u>	not bound
8a, SEQ. ID NO. 27	U <u>A</u> UUUUUU	not bound
8b, SEQ. ID NO. 28	UAUUUUUU <u>C</u>	not bound
8c, SEQ. ID NO. 29	UAUUUU <u>C</u> U	not bound
5, SEQ. ID NO. 30	UAUU <u>A</u> UUU	1.14 +/- 0.24
6, SEQ. ID NO. 31	<u>A</u> AUUUAUUU	1.01 +/- 0.27
MOTIF	NNUUNNUU	

Line 7, page 25:

TABLE 1:

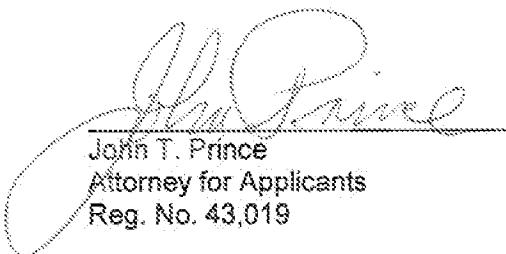
Name	Sequence	Position
Openers SEQ. ID NO. 32	O <sub>1</sub> AATATAAAATTAAATATT	804-823
SEQ. ID NO. 33	O <sub>2</sub> TAGAGCCCTAGGGCTTACA	909-928
Negative Controls SEQ. ID NO. 34	N <sub>1</sub> AGTGGGAAGCACTTAATTAC	757-775
SEQ. ID NO. 35	N <sub>2</sub> CATAATAATAATTTTGG	969-980

**f) Quantitative real-time RT PCR**

RNA is reverse transcribed to cDNA using the TaqMan RT PCR reagents (Applied Biosystems) and random hexamers for priming following standard protocols. Quantitative RT-PCR is performed with SYBR Green detection on an ABI7700 instrument (Applied Biosystems) with IL-2 specific primers SEQ. ID NO. 36: (forward: 5'-TCACCAGGATGCTCACATTAAGTT-3'; reverse: 5'-GGAGTTGAGTTCTTCTTAGACACTGA-3'; primers are a gift from F. Kalthoff, Novartis Institute for Biomedical Research Vienna). EF-1 alpha is used as endogenous control for normalization (primers: forward SEQ. ID NO. 37: 5'-TTTGAGACCAGCAAGTACTATGTGACT-3'; reverse 5'-TCAGCCTGAGATGTCCCTGTAA-3'). The  $\Delta\Delta Ct$  method is used for relative quantification of IL-2 mRNA levels (as described by Applied Biosystems). All presented data are averages from at least 5 identical independent samples and representative of at least two independent experiments using cells from different donors.

Applicant submits that no new material is being added and the amended tables and line amendments bring the specification into conformance with the sequence listing submitted in Response to the Notice of Missing Requirements mailed June 10, 2008.

Respectfully submitted,

  
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